Listing of Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Previously Presented) A method for analysing a heterogeneous sample of proteins, peptides or fragments thereof, the method comprising:

   (a) separating the heterogeneous sample of proteins, peptides or fragments thereof into heterogeneous classes by binding members of each class to a spaced apart defined location on an array, wherein members of each class have a motif common to that class; and

   (b) characterising the proteins, peptides or fragments thereof in each class.

2. (Original) A method according to Claim 1 wherein the heterogeneous sample of proteins or peptides is an extract of the total protein content of a cell or tissue type.

3. (Previously Presented) A method according to Claim 1 wherein, prior to performing step (a), the heterogeneous sample of fragments is formed by fragmenting a heterogeneous sample of proteins or peptides.

4. (Original) A method according to Claim 3 wherein the fragmenting is performed by chemical or enzymatic cleavage.

5. (Previously Presented) A method according to Claim 3 wherein the fragmenting is performed using a sequence-directed cleavage mechanism.

6. (Previously Presented) A method according to Claim 3 wherein the fragmenting is performed by digestion of the heterogeneous sample of proteins or peptides with trypsin.

7. (Previously Presented) A method according to claim 1 wherein the motif in each protein, peptide or fragment thereof is at the same location in each protein, peptide or fragment thereof, relative to the C-terminus, the N-terminus, or an internal feature.

8. (Previously Presented) A method according to claim 1 wherein the sample is a heterogeneous sample of fragments of proteins or peptides and the motif in each fragment is at the same location in each fragment, relative to the site of cleavage.

9. (Previously Presented) A method according to claim 1 wherein the motif in each protein, peptide or fragment thereof is three, four, five, six or more amino acids in length.

10. (Previously Presented) A method according to claim 1 wherein the motif contains three, four or five variable amino acids, the other amino acids in the motif being constant between all proteins, peptides or fragments

thereof.

11. (Previously Presented) A method according claim 1 wherein the motif is at the C-terminus.

12. (Previously Presented) A method according to claim 1 wherein the motif is at the N-terminus.

13. (Previously Presented) A method according to claim 1 wherein the array comprises a number of different types of binding molecule, each type immobilised at a spaced apart defined location on the array, wherein each type of binding molecule is capable of binding specifically to a motif and wherein different types of binding molecule have different binding specificities.

14. (Previously Presented) A method according to Claim 13 wherein the number of different types of binding molecule provided on the array is suitable to capture at least 10% of the proteins or peptides in the unfragmented sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment from at least 10% of the proteins or peptides in the unfragmented sample.

15. (Previously Presented) A method according to Claim 13 wherein the number of different types of binding molecule provided on the array is suitable to capture at least 50% of the proteins or peptides in the unfragmented sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment

from at least 50% of the proteins or peptides in the unfragmented sample.

16. (Previously Presented) A method according to Claim 13 wherein the number of different types of binding molecule provided on the array is suitable to capture substantially 100% of the proteins or peptides in the unfragmented sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment from substantially 100% of the proteins or peptides in the unfragmented sample.

17. (Previously Presented) A method according to claim 13 wherein the array has at least about 10, 50, 100, 150, 200, 250, 300, or more different types of binding molecules provided thereon.

18. (Previously Presented) A method according to claim 13 wherein at least one type of the binding molecule is an antibody or a fragment or variant thereof.

19. (Previously Presented) A method according to claim 13 wherein at least one of the types of the binding molecule is an aptamer.

20. (Previously Presented) A method according to claim 13 wherein at least one of the types of the binding molecule is a polynucleotide.

21. (Previously Presented) A method according to claim 1 wherein step (b) comprises characterising bound proteins,

peptides or fragments thereof at the defined and discrete locations on the array.

22. (Previously Presented) A method according to claim 1 wherein step (b) comprises determining the mass of proteins, peptides or fragments thereof in the heterogeneous classes.

23. (Previously Presented) A method according to Claim 22 wherein step (b) further comprises determining the abundance of proteins, peptides or fragments thereof of different mass in the heterogeneous classes.

24. (Previously Presented) A method according to claim 1 wherein step (b) comprises characterising the proteins, peptides or fragments thereof in the heterogeneous classes by desorption mass spectrometry or collision induced dissociation mass spectrometry.

25. (Previously Presented) A method according to claim 1 wherein the information derived from step (b) is used to determine the identity of the parent protein or peptide in the unfragmented heterogeneous sample from which a detected peptide fragment is derived.

26. (Previously Presented) A method according to claim 1 wherein the information derived from step (b) is used to determine the abundance of a protein or peptide in the heterogeneous sample.

27. (Previously Presented) A method for identifying

differences in composition between two or more heterogeneous fragmented or unfragmented samples of proteins, peptides or fragments thereof comprising analysing each sample by the method according to claim 1 and comparing the results, thereby to identify any differences.

28. (Original) A method for identifying a disease-related protein or peptide comprising identifying differences between two or more samples by the method of Claim 27, wherein at least one of the samples analysed is derived from an individual with the disease and another one of the samples analysed is derived from a individual without the disease.

29. (Previously Presented) A method of diagnosing the disease state of an individual comprising analysing an ex vivo sample taken from the individual by a method according to claim 1 and determining whether the results correspond with a disease-related protein or peptide.

30. (Previously Presented) An array comprising a number of different types of binding molecule, each type immobilised at a defined and discrete location on the array, wherein each type of binding molecule is capable of binding specifically to a motif and wherein the different types of binding molecule have different binding specificities.

31. (Original) An array according to Claim 30 wherein the number of different types of binding molecule provided on

the array is such that, when a heterogeneous sample of proteins, or peptides or fragments thereof, is applied to the array, at least 10%, 50% or substantially 100% of the proteins or peptides in the sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment from at least 10%, 50% or substantially 100% of the proteins or peptides in the unfragmented sample is captured on the array.

32. (Previously Presented) An array according to Claim 30 wherein the number of different types of binding molecule provided on the array is at least about 10, 50, 100, 150, 200, 250, 300, or more.

33. (Previously Presented) An array according to claim 30 wherein at least one type of the binding molecule is an antibody or a fragment or variant thereof, an aptamer, or a polynucleotide.

34. (Previously Presented) A method of producing an array suitable for use in a method according to claim 1 comprising:

(a) providing a library of different types of binding molecule, each type being capable of binding specifically to a motif and the different types having different binding specificity; and

(b) immobilising the binding molecules on an array such that different types of binding molecule are immobilised at defined and discrete locations.

35. (Previously Presented) A method according Claim 34 wherein the library of different type of binding molecule comprises at least one type of binding molecule which is an antibody or a fragment or variant thereof, an aptamer or a polynucleotide.

36. (Previously Presented) An array obtainable by the method of Claim 34.

37. (Previously Presented) A system for analysing a heterogeneous sample of proteins or peptides, the system comprising an array according to claim 30 and a data carrier comprising information on the identity and/or binding property and position of each different type of binding molecule on the array.

38. (Canceled)

39. (Canceled)

40. (Previously Presented) A library of at least about 10, 50, 100, 150, 200, 250, 300, or more different types of binding molecule, each type being capable of binding specifically to a motif and the different types having different binding specificities.

41. (Previously Presented) A library according to Claim 40 wherein at least one type of binding molecule is an antibody or a fragment or variant thereof, an aptamer, or a polynucleotide.

42. (Previously Presented) A method for making a library of binding molecules comprising:

(a) providing, as a first component, a selector peptide comprising a motif;

(b) providing, as a second component, a source of candidate binding molecules;

(c) combining the first and second components; and

(d) identifying candidate binding molecules that are capable of specifically binding to the motif of the selector peptide in the first component.

43. (Original) A library of at least about 10, 50, 100, 150, 200, 250, 300, or more different types of binding molecules obtainable by the method of Claim 42.

44. (Canceled)

45. (Previously Presented) A data carrier comprising information obtainable by a method according to claim 1.

46. (Previously Presented) An electronic data processing system comprising a data carrier according to Claim 45 and means of comparing information obtainable from the analysis of different samples.

47. (Canceled)

48. (Previously Presented) A method of treating an individual identified as being in need thereof by a method according to Claim 29 comprising administering an effective amount of a pharmaceutical agent appropriate to the disease state of the individual.

49. (Previously Presented) A method for making a library of binding molecules comprising:

(a) providing, as a first component, a selector peptide comprising a motif;

(b) providing, as a second component, a source of candidate binding molecules;

(c) combining the first and second components;

(d) identifying candidate binding molecules that are capable of specifically binding to the motif of the selector peptide in the first component;

(e) immobilising the binding molecules identified in step (d) on an array such that different types of binding molecule are immobilised at defined and discrete locations;

(f) providing a heterogeneous sample of proteins, peptides or fragments thereof, which sample comprises proteins, peptides or fragments thereof

each having a motif that is bound by a binding molecule immobilised in step (e);

(g) separating the heterogeneous sample of proteins, peptides or fragments thereof into heterogeneous classes by binding members of each class to the binding molecules immobilised in step (e); and

(h) characterising the proteins, peptides or fragments thereof in each class.